WHAT IS CLAIMED IS:

1. A method of increasing the hybridization rate between first and second nucleic acids in a diagnostic hybridization assay for use in detecting the presence or amount of at least one nucleic acid analyte, wherein a first nucleotide base sequence region of said first nucleic acid is able to stably hybridize to a first nucleotide base sequence region of said second nucleic acid under selective hybridization conditions, which comprises the steps of:

a) synthesizing at least one of said nucleotide regions to include one or more modified nucleotides, so that

i) the hybridization binding affinity between said first and second nucleic acids is greater than the hybridization binding affinity between unmodified forms of said first and second nucleic acids, under said conditions, and

ii) the hybridization rate between said first and second nucleic acids is greater than the hybridization rate between unmodified forms of said first and second nucleic acids, under said conditions; and

b) contacting said first and second nucleic acids of step a) under said conditions, such that said nucleotide regions are able to stably hybridize.

2. The method of claim 1, wherein said first and second nucleic acids are contained on the same nucleic acid strand.

3. The method of claim 1, wherein at least one of said nucleotide regions includes one or more clusters of at least about 4 modified nucleotides.

4. The method of claim 1, wherein at least one of said nucleotide regions includes one or more clusters of at least about 6 modified nucleotides.

5. The method of claim 1, wherein at least one of said nucleotide regions

includes one or more clusters of at least about 8 modified nucleotides.

6. The method of claim 1, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions are modified.

7. The method of claim 3, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

8. The method of claim 3, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage;

e) a modification to the internucleotide linkage.

9. The method of claim 3, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

10. The method of claim 3, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

11. The method of claim 3, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

12. The method of claim 11, wherein said propyne substitution is to a cytidine analog.

13. The method of claim 11, wherein said propyne substitution is to a thymidine analog.

14. The method of claim 3, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions contains the same modification.

15. The method of claim 14, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

16. The method of claim 1, wherein at least one of said nucleic acids includes one or more conjugate molecules.

17. The method of claim 3, wherein at least one of said nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions.

18. The method of claim 3, wherein said first nucleotide region of said first

nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

19. The method of claim 18, wherein said first nucleic acid comprises an oligonucleotide probe.

20. The method of claim 19, wherein said probe consists of from about 10 to about 100 nucleotide bases.

21. The method of claim 19, wherein said probe consists of from about 10 to about 16 nucleotide bases.

22. The method of claim 19, wherein said probe consists of from about 12 to about 16 nucleotide bases.

23. The method of claim 19, wherein said probe further includes a label.

24. The method of claim 23, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to said second nucleic acid under said conditions.

25. The method of claim 24, wherein said label is a chemiluminescent molecule.

26. The method of claim 25, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

27. The method of claim 25, wherein said chemiluminescent molecule is an acridinium ester derivative.

28. The method of claim 23, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

29. The method of claim 19, wherein said second nucleic acid comprises said analyte.

30. The method of claim 29, wherein said analyte consists of RNA.

31. The method of claim 30, wherein said RNA consists of rRNA or tRNA.

32. The method of claim 29, wherein said analyte consists of DNA.

33. The method of claim 3, wherein each said nucleotide region includes one or more clusters of at least about 4 modified nucleotides.

34. The method of claim 33, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions contains the same modification.

35. The method of claim 34, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

36. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region that is able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions, and wherein said first nucleotide region of said probe includes one or more modified nucleotides;

b) subjecting the components of step a) to said conditions, so that

i) the hybridization binding affinity between said analyte and said probe is greater than the hybridization binding affinity between said analyte and an unmodified form of said probe, under said conditions, and

ii) the hybridization rate between said analyte and said probe is greater than the hybridization rate between said analyte and an unmodified form of said probe, under said conditions; and

c) detecting said probe hybridized to said analyte as an indication of the presence or amount of said analyte in said sample.

37. The method of claim 36, wherein said first nucleotide region of said probe includes one or more clusters of at least about 4 modified nucleotides.

38. The method of claim 36, wherein said first nucleotide region of said probe includes one or more clusters of at least about 6 modified nucleotides.

39. The method of claim 36, wherein said first nucleotide region of said probe includes one or more clusters of at least about 8 modified nucleotides.

40. The method of claim 36, wherein substantially all of the nucleotides contained in said first nucleotide region of said probe are modified.

41. The method of claim 37, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

42. The method of claim 37, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

43. The method of claim 37, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

44. The method of claim 37, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

45. The method of claim 37, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

46. The method of claim 45, wherein said propyne substitution is to a cytidine analog.

47. The method of claim 45, wherein said propyne substitution is to a thymidine analog.

48. The method of claim 37, wherein each said modified nucleotide of one or more of said clusters contains the same modification.

49. The method of claim 48, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

50. The method of claim 36, wherein said probe includes one or more conjugate molecules.

51. The method of claim 37, wherein said probe includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to said probe at a site located within one or more of said clusters contained in said first nucleotide

region of said probe.

52. The method of claim 37, wherein said probe is an oligonucleotide consisting of from about 10 to about 100 nucleotide bases.

53. The method of claim 37, wherein said probe is an oligonucleotide consisting of from about 10 to about 16 nucleotide bases.

54. The method of claim 37, wherein said probe is an oligonucleotide consisting of from about 12 to about 16 nucleotide bases.

55. The method of claim 37, wherein said probe further includes a label.

56. The method of claim 55, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a nucleotide base sequence region that is unable to stably hybridize to said analyte under said conditions.

57. The method of claim 56, wherein said label is a chemiluminescent molecule.

58. The method of claim 57, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

59. The method of claim 57, wherein said chemiluminescent molecule is an acridinium ester derivative.

60. The method of claim 55, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

61. The method of claim 37, wherein said analyte consists of RNA.

62. The method of claim 61, wherein said RNA is rRNA or tRNA.

63. The method of claim 61, wherein said sample further contains DNA.

64. The method of claim 37, wherein said analyte consists of DNA.

65. The method of either claim 37 or 55, wherein said probe or said analyte is directly or indirectly immobilized by a solid support.

66. The method of claim 36, wherein said contacting step further includes contacting said probe with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to either said third nucleic acid or said second nucleotide region of said probe under said conditions, and

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said probe under said conditions.

67. The method of claim 66, wherein at least one of said nucleotide regions of said probe and said third nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

68. The method of claim 66, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third nucleic acid are modified.

69. The method of claim 67, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

70. The method of claim 67, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said third nucleic acid contains the same modification.

71. The method of claim 70, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

72. The method of claim 66, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules.

73. The method of claim 67, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules, and wherein at least one of said

conjugate molecules is joined to at least one of said probe and said third nucleic acid at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third nucleic acid.

74. The method of claim 67, wherein said probe further includes a label.

75. The method of claim 74, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a nucleotide base sequence region that is unable to stably hybridize to either said analyte or said third nucleic acid under said conditions.

76. The method of claim 75, wherein said label is a chemiluminescent molecule.

77. The method of claim 76, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

78. The method of claim 76, wherein said label is an acridinium ester derivative.

79. The method of claim 67, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

80. The method of claim 67, wherein said analyte consists of RNA.

81. The method of either claim 67 or 74, wherein one of said analyte and said third nucleic acid is directly or indirectly immobilized by a solid support.

82. The method of claim 36, wherein said contacting step further includes contacting said analyte with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions,

wherein said probe is unable to stably hybridize to either said third nucleic acid or said second nucleotide region of said analyte under said conditions, and

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said analyte under said conditions.

83. The method of claim 82, wherein at least one of said nucleotide regions of said probe and said third nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

84. The method of claim 82, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third nucleic acid are modified.

85. The method of claim 83, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

86. The method of claim 83, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said third nucleic acid contains the same modification.

87. The method of claim 86, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

88. The method of claim 82, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules.

89. The method of claim 83, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said third nucleic acid at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third nucleic acid.

90. The method of claim 83, wherein said third nucleic acid is a helper probe.

91. The method of claim 83, wherein said probe further includes a label.

92. The method of claim 91, wherein said label is selected from the group consisting of:

a) a radioisotope,

b) an enzyme,

c) an enzyme cofactor,

d) an enzyme substrate,

e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to either said analyte or said third nucleic acid under said conditions.

93. The method of claim 92, wherein said label is a chemiluminescent molecule.

94. The method of claim 93, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

95. The method of claim 93, wherein said label is an acridinium ester derivative.

96. The method of claim 91, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

97. The method of claim 83, wherein said analyte consists of RNA.

98. The method of either claim 83 or 91, wherein one of said probe and

said third nucleic acid is directly or indirectly immobilized by a solid support.

99. The method of claim 36, wherein said contacting step further includes contacting a third nucleic acid with said analyte and said probe, wherein said third nucleic acid contains:

a) a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions; and

b) a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions,

wherein said analyte is not able to stably hybridize to either said second nucleotide region of said probe or said second nucleotide region of said third nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to either said second nucleotide region of said analyte or said first nucleotide region of said third nucleic acid under said conditions, and

wherein said third nucleic acid is unable to stably hybridize to either said first nucleotide region of said analyte or said first nucleotide region of said probe.

100. The method of claim 99, wherein at least one of said nucleotide regions of said probe and said third nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

101. The method of claim 99, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third nucleic acid are modified.

102. The method of claim 100, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

103. The method of claim 100, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said third nucleic acid contains the same modification.

104. The method of claim 103, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

105. The method of claim 99, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules.

106. The method of claim 100, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said third nucleic acid at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third nucleic acid.

107. The method of claim 100, wherein said probe further includes a label.

108. The method of claim 107, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to either said analyte or said third nucleic acid under said conditions.

109. The method of claim 108, wherein said label is a chemiluminescent molecule.

110. The method of claim 109, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

111. The method of claim 109, wherein said label is an acridinium ester derivative.

112. The method of claim 100, wherein said analyte consists of RNA.

113. The method of either claim 100 or 107, wherein one of said probe and said third nucleic acid is directly or indirectly immobilized by a solid support.

114. The method of claim 36, wherein said contacting step further includes contacting the following components:

a) said probe with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second

nucleotide base sequence region of said probe under selective hybridization conditions; and

b) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said third nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe and said third and fourth nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to either of said second nucleotide region of said third nucleic acid and said fourth nucleic acid under said conditions,

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said probe under said conditions, and

wherein said fourth nucleic acid is unable to stably hybridize to said first nucleotide region of said third nucleic acid under said conditions.

115. The method of claim 114, wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

116. The method of claim 114, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids are modified.

117. The method of claim 115, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

118. The method of claim 115, wherein each said modified nucleotide of one or more of said clusters of at least one of said probe and said third and fourth nucleic acids contains the same modification.

119. The method of claim 118, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

120. The method of claim 114, wherein at least one of said probe and said third and fourth nucleic acids includes one or more conjugate molecules.

121. The method of claim 115, wherein at least one of said probe and said third and fourth nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said third and fourth nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids.

122. The method of claim 115, wherein said probe further includes a label.

123. The method of claim 122, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a nucleotide base sequence region that is unable to stably

hybridize to any of said analyte and said third and fourth nucleic acids under said conditions.

124. The method of claim 123, wherein said label is a chemiluminescent molecule.

125. The method of claim 124, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

126. The method of claim 124, wherein said label is an acridinium ester derivative.

127. The method of claim 122, wherein said label is joined to said probe at a site located within one of said clusters of said first nucleotide region of said probe.

128. The method of claim 115, wherein said analyte consists of RNA.

129. The method of either claim 115 or 122, wherein said fourth nucleic acid is immobilized by a solid support.

130. The method of claim 36, wherein said contacting step further includes contacting the following components:

a) said analyte with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions; and

b) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said third nucleic acid under selective

hybridization conditions,

wherein said analyte is unable to stably hybridize to either said second nucleotide region of said third nucleic acid or said fourth nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte and said third and fourth nucleic acids under said conditions,

wherein said third nucleic acid is unable to stably hybridize to either said first nucleotide region of said analyte or said probe under said conditions, and

wherein said fourth nucleic acid is unable to stably hybridize to said first nucleotide region of said third nucleic acid under said conditions.

131. The method of claim 130, wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

132. The method of claim 130, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids are modified.

133. The method of claim 131, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

134. The method of claim 131, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said third and fourth nucleic acids contains the same modification.

135. The method of claim 134, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

136. The method of claim 130, wherein at least one of said probe and said third and fourth nucleic acids includes one or more conjugate molecules.

137. The method of claim 131, wherein at least one of said probe and said third and fourth nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said third and fourth nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids.

138. The method of claim 131, wherein said probe further includes a label.

139. The method of claim 138, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a nucleotide base sequence region that is unable to stably hybridize to any of said analyte and said third and fourth nucleic acids under said conditions.

140. The method of claim 139, wherein said label is a chemiluminescent

molecule.

141. The method of claim 140, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

142. The method of claim 140, wherein said label is an acridinium ester derivative.

143. The method of claim 138, wherein said label is joined to said probe at a site located within one of said clusters of said first nucleotide region of said probe.

144. The method of claim 131, wherein said analyte consists of RNA.

145. The method of either claim 131 or 138, wherein said fourth nucleic acid is immobilized by a solid support.

146. The method of claim 36, wherein said contacting step further includes contacting the following components:

a) said analyte with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions;

b) said probe with said third nucleic acid, wherein said third nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions; and

c) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a third nucleotide base sequence region of said third nucleic acid under selective hybridization

conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe, said second and third nucleotide regions of said third nucleic acid, and said fourth nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte, said first and third nucleotide regions of said third nucleic acid, and said fourth nucleic acid under said conditions,

wherein said third nucleic acid is unable to stably hybridize to either said first nucleotide region of said analyte or said first nucleotide region of said probe under said conditions, and

wherein said fourth nucleic acid is unable to stably hybridize to either said first or second nucleotide region of said third nucleic acid under said conditions.

147. The method of claim 146, wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

148. The method of claim 146, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids are modified.

149. The method of claim 147, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

150. The method of claim 147, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said third and fourth nucleic acids contains the same modification.

151. The method of claim 150, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

152. The method of claim 146, wherein at least one of said probe and said third and fourth nucleic acids includes one or more conjugate molecules.

153. The method of claim 147, wherein at least one of said probe and said third and fourth nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said third and fourth nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids.

154. The method of claim 147, wherein said probe further includes a label.

155. The method of claim 154, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a nucleotide base sequence region that is unable to stably

hybridize to any of said analyte and said third and fourth nucleic acids under said conditions.

156. The method of claim 155, wherein said label is a chemiluminescent molecule.

157. The method of claim 156, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

158. The method of claim 156, wherein said label is an acridinium ester derivative.

159. The method of claim 154, wherein said label is joined to said probe at a site located within one of said clusters of said first nucleotide region of said probe.

160. The method of claim 147, wherein said analyte consists of RNA.

161. The method of either claim 147 or 154, wherein said fourth nucleic acid is immobilized by a solid support.

162. The method of claim 36, wherein said contacting step further includes contacting the following components:

a) said probe with a first coupling nucleic acid comprising a third nucleic acid, wherein said first coupling nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions;

b) a second coupling nucleic acid comprising a fourth nucleic acid with a fifth nucleic acid, wherein said fifth nucleic acid contains a first nucleotide base

sequence region able to stably hybridize to a first nucleotide base sequence region of said second coupling nucleic acid under selective hybridization conditions; and, alternatively,

i) said first coupling nucleic acid with said second coupling nucleic acid, wherein said second coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said first coupling nucleic acid under selective hybridization conditions; or

ii) one or more optional coupling nucleic acids, other than said first and second coupling nucleic acids, wherein each of said optional coupling nucleic acids can stably hybridize to at least two other coupling nucleic acids under selective hybridization conditions, wherein at least one of said other coupling nucleic acids may be at least one of said first and second coupling nucleic acids, and wherein each of said other coupling nucleic acids is directly or indirectly joined to said fifth nucleic acid and said analyte,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and said optional coupling nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and said optional coupling nucleic acids under said conditions,

wherein said first coupling nucleic acid is unable to stably hybridize to any of said first nucleotide region of said probe, said first nucleotide region of said second coupling nucleic acid, and said fifth nucleic acid under said conditions,

wherein said second coupling nucleic acid is unable to stably hybridize to said first nucleotide region of said first coupling nucleic acid under said conditions,

wherein said fifth nucleic acid is unable to stably hybridize to either said second nucleotide region of said second coupling nucleic acid or said optional coupling nucleic acids under said conditions, and

wherein said optional coupling nucleic acids do not stably hybridize to said

first nucleotide region of either said first or second coupling nucleic acid under said conditions.

163. The method of claim 162, wherein at least one of said nucleotide regions of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and a nucleotide base sequence region of any one of said optional coupling nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

164. The method of claim 162, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and a nucleotide base sequence region of any one of said optional coupling nucleic acids are modified.

165. The method of claim 163, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

166. The method of claim 163, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe, said fifth nucleic acid, and any of said coupling nucleic acids contains the same modification.

167. The method of claim 166, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

168. The method of claim 162, wherein at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids includes one or more conjugate molecules.

169. The method of claim 163, wherein at least one of said probe, said fifth

nucleic acid, and any of said coupling nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe, said fifth nucleic acid, and any of said coupling nucleic acids.

170. The method of claim 163, wherein said probe further includes a label.

171. The method of claim 170, wherein said label is selected from the group consisting of:

a) a radioisotope,

b) an enzyme,

c) an enzyme cofactor,

d) an enzyme substrate,

e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to any of said analyte, said fifth nucleic acid, and said coupling nucleic acids under said conditions.

172. The method of claim 171, wherein said label is a chemiluminescent molecule.

173. The method of claim 172, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

174. The method of claim 172, wherein said label is an acridinium ester derivative.

175. The method of claim 170, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

176. The method of claim 163, wherein said analyte consists of RNA.

177. The method of either claim 163 or 170, wherein said fifth nucleic acid is immobilized by a solid support.

178. The method of claim 36, wherein said contacting step further includes contacting the following components:

a) said analyte with a first coupling nucleic acid comprising a third nucleic acid, wherein said first coupling nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions;

b) a second coupling nucleic acid comprising a fourth nucleic acid with a fifth nucleic acid, wherein said fifth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said second coupling nucleic acid under selective hybridization conditions; and, alternatively,

i) said first coupling nucleic acid with said second coupling nucleic acid, wherein said second coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said

first coupling nucleic acid under selective hybridization conditions; or

ii) one or more optional coupling nucleic acids, other than said first and second coupling nucleic acids, wherein each of said optional coupling nucleic acids is able to stably hybridize to two other coupling nucleic acids under selective hybridization conditions, wherein at least one of said other coupling nucleic acids may be at least one of said first and second coupling nucleic acids, and wherein each of said other coupling nucleic acids is directly or indirectly joined to said fifth nucleic acid and said analyte,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and said optional coupling nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte, said first and second coupling nucleic acids, said fifth nucleic acid, and said optional coupling nucleic acids under said conditions,

wherein said first coupling nucleic acid is unable to stably hybridize to any of said first nucleotide region of said analyte, said first nucleotide region of said second coupling nucleic acid, and said fifth nucleic acid under said conditions,

wherein said second coupling nucleic acid is unable to stably hybridize to said first nucleotide region of said first coupling nucleic acid under said conditions,

wherein said fifth nucleic acid is unable to stably hybridize to either said second nucleotide region of said second coupling nucleic acid or said optional coupling nucleic acids under said conditions, and

wherein said optional coupling nucleic acids do not stably hybridize to said first nucleotide region of either said first or second coupling nucleic acid under said conditions.

179. The method of claim 178, wherein at least one of said nucleotide regions of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and

a nucleotide base sequence region of any one of said optional coupling nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

180. The method of claim 178, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and a nucleotide base sequence region of any one of said optional coupling nucleic acids are modified.

181. The method of claim 179, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

182. The method of claim 179, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe, said fifth nucleic acid, and any of said coupling nucleic acids contains the same modification.

183. The method of claim 182, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

184. The method of claim 178, wherein at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids includes one or more conjugate molecules.

185. The method of claim 179, wherein at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe, said fifth nucleic acid, and any of said coupling nucleic acids.

186. The method of claim 179, wherein said probe further includes a label.

187. The method of claim 186, wherein said label is selected from the group consisting of:

a) a radioisotope,

b) an enzyme,

c) an enzyme cofactor,

d) an enzyme substrate,

e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to any of said analyte, said fifth nucleic acid, and any of said coupling nucleic acids under said conditions.

188. The method of claim 187, wherein said label is a chemiluminescent molecule.

189. The method of claim 188, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

190. The method of claim 188, wherein said label is an acridinium ester derivative.

191. The method of claim 186, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

192. The method of claim 179, wherein said analyte consists of RNA.

193. The method of either claim 179 or 186, wherein said fifth nucleic acid is immobilized by a solid support.

194. The method of claim 36, wherein said contacting step further includes contacting the following components:

a) said probe with a first coupling nucleic acid comprising a third nucleic acid, wherein said first coupling nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions;

b) said analyte with said first coupling nucleic acid, wherein said first coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions;

c) a second coupling nucleic acid comprising a fourth nucleic acid with a fifth nucleic acid, wherein said fifth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said second coupling nucleic acid under selective hybridization conditions; and, alternatively,

i) said first coupling nucleic acid with said second coupling nucleic acid, wherein said second coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a third nucleotide base sequence region of said first coupling nucleic acid under selective hybridization conditions; or

ii) one or more optional coupling nucleic acids, other than said first and second coupling nucleic acids, wherein each of said optional coupling nucleic

acids is able to stably hybridize to two other coupling nucleic acids under selective hybridization conditions, wherein at least one of said other coupling nucleic acids may be at least one of said first and second coupling nucleic acids, and wherein each of said other coupling nucleic acids is directly or indirectly joined to said analyte, said probe and said fifth nucleic acid,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe, said first and third nucleotide regions of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and said optional coupling nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte, said second and third nucleotide regions of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and said optional coupling nucleic acids under said conditions,

wherein said first coupling nucleic acid is unable to stably hybridize to any of said first nucleotide region of said analyte, said first nucleotide region of said probe, said first nucleotide region of said second coupling nucleic acid, and said fifth nucleic acid under said conditions,

wherein said second coupling nucleic acid is unable to stably hybridize to either said first or second nucleotide region of said first coupling nucleic acid under said conditions,

wherein said fifth nucleic acid is unable to stably hybridize to either said second nucleotide region of said second coupling nucleic acid or said optional coupling nucleic acids under said conditions, and

wherein said optional coupling nucleic acids do not stably hybridize to any of said first and second nucleotide regions of said first coupling nucleic acid and said first nucleotide region of said second coupling nucleic acid under said conditions.

195. The method of claim 194, wherein at least one of said nucleotide

regions of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and a nucleotide base sequence region of any of said optional coupling nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

196. The method of claim 194, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and a nucleotide base sequence region of any of said optional coupling nucleic acids are modified.

197. The method of claim 195, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

198. The method of claim 195, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe, said fifth nucleic acid, and any of said coupling nucleic acids contains the same modification.

199. The method of claim 198, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

200. The method of claim 194, wherein at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids includes one or more conjugate molecules.

201. The method of claim 195, wherein at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe, said fifth nucleic acid, and any of said coupling nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said

probe, said fifth nucleic acid, and any of said coupling nucleic acids.

202. The method of claim 195, wherein said probe further includes a label.

203. The method of claim 202, wherein said label is selected from the group consisting of:

a) a radioisotope,

b) an enzyme,

c) an enzyme cofactor,

d) an enzyme substrate,

e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to any of said analyte, said fifth nucleic acid, and said coupling nucleic acids under said conditions.

204. The method of claim 203, wherein said label is a chemiluminescent molecule.

205. The method of claim 204, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

206. The method of claim 204, wherein said label is an acridinium ester derivative.

207. The method of claim 202, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

208. The method of claim 195, wherein said analyte consists of RNA.

209. The method of either claim 195 or 202, wherein said fifth nucleic acid is immobilized by a solid support.

210. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting the following components:

i) said sample with a second nucleic acid, wherein said second nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions; and

ii) a probe comprising a third nucleic acid with said second nucleic acid, wherein said second nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said probe under selective hybridization conditions,

wherein said second nucleic acid cannot stably hybridize to said probe unless said second nucleic acid is stably hybridized with said analyte,

wherein said analyte is unable to stably hybridize to either said probe or said second nucleotide region of said second nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to said first nucleotide region

of said second nucleic acid under said conditions,

wherein said second nucleic acid is unable to stably hybridize to said first nucleotide region of said analyte under said conditions, and

wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more modified nucleotides;

b) subjecting the components of step a) to selective hybridization conditions, so that

if at least one of said first nucleotide region of said probe and said second nucleotide region of said second nucleic acid includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said probe and said second nucleic acid is greater than the hybridization binding affinity between unmodified forms of said probe and said second nucleic acid, under identical hybridization conditions, and

ii) the hybridization rate between said probe and said second nucleic acid is greater than the hybridization rate between unmodified forms of said probe and said second nucleic acid, under identical hybridization conditions, and

if said first nucleotide region of said second nucleic acid includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said analyte and said second nucleic acid is greater than the hybridization binding affinity between said analyte and an unmodified form of said second nucleic acid, under identical hybridization conditions, and

ii) the hybridization rate between said analyte and said second nucleic acid is greater than the hybridization rate between said analyte and an unmodified form of said second nucleic acid, under identical hybridization conditions; and

c) detecting said labeled probe hybridized with said second nucleic acid as an indication of the presence or amount of said analyte in said sample.

211. The method of claim 210, wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

212. The method of claim 210, wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more clusters of at least about 6 modified nucleotides.

213. The method of claim 210, wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more clusters of at least about 8 modified nucleotides.

214. The method of claim 210, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said second nucleic acid are modified.

215. The method of claim 211, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

216. The method of claim 211, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

217. The method of claim 211, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

218. The method of claim 211, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

219. The method of claim 211, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

220. The method of claim 219, wherein said propyne substitution is to a cytidine analog.

221. The method of claim 219, wherein said propyne substitution is to a thymidine analog.

222. The method of claim 211, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said second nucleic acid contains the same modification.

223. The method of claim 222, wherein said modification consists of a 2'-O-

methyl substitution to the ribofuranosyl moiety.

224. The method of claim 210, wherein at least one of said probe and said second nucleic acid includes one or more conjugate molecules.

225. The method of claim 211, wherein at least one of said probe and said second nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said second nucleic acid at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said second nucleic acid.

226. The method of claim 211, wherein said probe is an oligonucleotide consisting of from about 10 to about 100 nucleotide bases.

227. The method of claim 211, wherein said probe is an oligonucleotide consisting of from about 10 to about 16 nucleotide bases.

228. The method of claim 211, wherein said probe is an oligonucleotide consisting of from about 12 to about 16 nucleotide bases.

229. The method of claim 211, wherein said probe further includes a label.

230. The method of claim 229, wherein said label is selected from the group consisting of:

a) a radioisotope,

b) an enzyme,

c) an enzyme cofactor,

d) an enzyme substrate,

e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to either said analyte or said second nucleic acid under said conditions.

231. The method of claim 230, wherein said label is a chemiluminescent molecule.

232. The method of claim 231, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

233. The method of claim 231, wherein said chemiluminescent molecule is an acridinium ester derivative.

234. The method of claim 229, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

235. The method of claim 211, wherein said analyte consists of RNA.

236. The method of claim 235, wherein said RNA is rRNA or tRNA.

237. The method of claim 235, wherein said sample further contains DNA.

238. The method of claim 211, wherein said analyte consists of DNA.

239. The method of either claim 211 or 229, wherein at least one of said analyte, said probe and said second nucleic acid is directly or indirectly immobilized by a solid support.

240. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said analyte with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions; and

iii) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said third nucleic acid under selective hybridization conditions,

wherein said third nucleic acid cannot stably hybridize to said fourth nucleic acid unless said third nucleic acid is stably hybridized with said analyte,

wherein said analyte is unable to stably hybridize to either said second nucleotide region of said third nucleic acid or said fourth nucleic acid under said conditions,

wherein said probe is unable to stably hybridize any of said second nucleotide region of said analyte and said third and fourth nucleic acids under said conditions,

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said analyte under said conditions,

wherein said fourth nucleic acid is unable to stably hybridize to said first nucleotide region of said third nucleic acid under said conditions, and

wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more modified nucleotides;

b) subjecting the components of step (a) to selective hybridization conditions, so that

if said first nucleotide region of said probe includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said analyte and said probe is greater than the hybridization binding affinity between said analyte and an unmodified form of said probe, under identical hybridization conditions, and

ii) the hybridization rate between said analyte and said probe is greater than the hybridization rate between said analyte and an unmodified form of said probe, under identical hybridization conditions,

if said first nucleotide region of said third nucleic acid includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said analyte and said third nucleic acid is greater than the hybridization binding affinity between said analyte and an unmodified form of said third nucleic acid, under identical hybridization conditions, and

ii) the hybridization rate between said analyte and said third nucleic acid is greater than the hybridization rate between said analyte and an unmodified form of said third nucleic acid, under identical hybridization conditions,

if at least one of said second nucleotide region of said third nucleic acid and said first nucleotide region of said fourth nucleic acid includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said third and fourth nucleic acids is greater than the hybridization binding affinity between unmodified forms of said third and fourth nucleic acids, under identical hybridization conditions, and

ii) the hybridization rate between said third and fourth nucleic acids is greater than the hybridization rate between unmodified forms of said third and fourth nucleic acids, under identical hybridization conditions; and

c) detecting said labeled probe hybridized with said analyte, as an indication of the presence or amount of said analyte in said sample.

241. The method of claim 240, wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more clusters of at least about 4 modified nucleotides.

242. The method of claim 240, wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more clusters of at least about 6 modified nucleotides.

243. The method of claim 240, wherein at least one of said nucleotide regions of said probe and said third and fourth nucleic acids includes one or more clusters of at least about 8 modified nucleotides.

244. The method of claim 240, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids are modified.

245. The method of claim 241, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

246. The method of claim 241, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

247. The method of claim 241, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

248. The method of claim 241, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

249. The method of claim 241, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

250. The method of claim 249, wherein said propyne substitution is to a cytidine analog.

251. The method of claim 249, wherein said propyne substitution is to a thymidine analog.

252. The method of claim 241, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said third and fourth nucleic acids contains the same modification.

253. The method of claim 252, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

254. The method of claim 240, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules.

255. The method of claim 241, wherein at least one of said probe and said third nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said third and fourth nucleic acids at a site located within one or more of said clusters contained in at least one of said nucleotide regions of said probe and said third and fourth nucleic acids.

256. The method of claim 241, wherein said probe is an oligonucleotide consisting of from about 10 to about 100 nucleotide bases.

257. The method of claim 241, wherein said probe is an oligonucleotide consisting of from about 10 to about 16 nucleotide bases.

258. The method of claim 241, wherein said probe is an oligonucleotide consisting of from about 12 to about 16 nucleotide bases.

259. The method of claim 241, wherein said probe further includes a label.

260. The method of claim 259, wherein said label is selected from the group consisting of:

a) a radioisotope,

b) an enzyme,

c) an enzyme cofactor,

d) an enzyme substrate,

e) a dye,

f) a hapten,

g) a chemiluminescent molecule,

h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to any of said analyte and said third and fourth nucleic acids under said conditions.

261. The method of claim 260, wherein said label is a chemiluminescent molecule.

262. The method of claim 261, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

263. The method of claim 261, wherein said chemiluminescent molecule is an acridinium ester derivative.

264. The method of claim 259, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

265. The method of claim 241, wherein said analyte consists of RNA.

266. The method of claim 265, wherein said RNA is rRNA or tRNA.

267. The method of claim 265, wherein said sample further contains DNA.

268. The method of claim 241, wherein said analyte consists of DNA.

269. The method of either claim 241 or 259, wherein said fourth nucleic acid is immobilized by a solid support.

270. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting the following components:

i) said sample with a second nucleic acid, wherein said second nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said analyte with a probe comprising a third nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions; and

iii) said probe with said second nucleic acid, wherein said second nucleic acid contains a second nucleotide base sequence region able to stably

hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions,

wherein said probe cannot stably hybridize to said analyte and said second nucleic acid unless said second nucleic acid is stably hybridized with said analyte,

wherein said analyte is unable to stably hybridize to either said second nucleotide region of said probe or said second nucleotide region of said second nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to either said first nucleotide region of said analyte or said first nucleotide region of said second nucleic acid under said conditions,

wherein said second nucleic acid is unable to stably hybridize to either said second nucleotide region of said analyte or said first nucleotide region of said probe under said conditions, and

wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more modified nucleotides;

b) subjecting the components of step a) to selective hybridization conditions, so that

if said first nucleotide region of said probe includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said analyte and said probe is greater than the hybridization binding affinity between said analyte and an unmodified form of said probe, under identical hybridization conditions, and

ii) the hybridization rate between said analyte and said probe is greater than the hybridization rate between said analyte and an unmodified form of said probe, under identical hybridization conditions,

if said first nucleotide region of said second nucleic acid includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said analyte

and said second nucleic acid is greater than the hybridization binding affinity between said analyte and an unmodified form of said second nucleic acid, under identical hybridization conditions, and

ii) the hybridization rate between said analyte and said second nucleic acid is greater than the hybridization rate between said analyte and an unmodified form of said second nucleic acid, under identical hybridization conditions, and

if at least one of said second nucleotide region of said probe and said second nucleotide region of said second nucleic acid includes one or more of said modified nucleotides, then

i) the hybridization binding affinity between said probe and said second nucleic acid is greater than the hybridization binding affinity between unmodified forms of said probe and said second nucleic acid, under identical hybridization conditions, and

ii) the hybridization rate between said probe and said second nucleic acid is greater than the hybridization rate between unmodified forms of said probe and said second nucleic acid, under identical hybridization conditions; and

c) detecting said labeled probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

271. The method of claim 270, wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

272. The method of claim 270, wherein at least one of said nucleotide regions of said probe and said second nucleic acid includes one or more clusters of at least about 6 modified nucleotides.

273. The method of claim 270, wherein at least one of said nucleotide

regions of said probe and said second nucleic acid includes one or more clusters of at least about 8 modified nucleotides.

274. The method of claim 270, wherein substantially all of the nucleotides contained in at least one of said nucleotide regions of said probe and said second nucleic acid are modified.

275. The method of claim 271, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

276. The method of claim 271, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

277. The method of claim 271, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

278. The method of claim 271, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

279. The method of claim 271, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

280. The method of claim 279, wherein said propyne substitution is to a cytidine analog.

281. The method of claim 279, wherein said propyne substitution is to a thymidine analog.

282. The method of claim 271, wherein each said modified nucleotide of one or more of said clusters of at least one of said nucleotide regions of said probe and said second nucleic acid contains the same modification.

283. The method of claim 282, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

284. The method of claim 270, wherein at least one of said probe and said second nucleic acid includes one or more conjugate molecules.

285. The method of claim 271, wherein at least one of said probe and said second nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said probe and said second nucleic acid at a site located within one or more of said clusters contained in at least one of said

nucleotide regions of said probe and said second nucleic acid.

286. The method of claim 271, wherein said probe is an oligonucleotide consisting of from about 10 to about 100 nucleotide bases.

287. The method of claim 271, wherein said probe is an oligonucleotide consisting of from about 10 to about 16 nucleotide bases.

288. The method of claim 271, wherein said probe is an oligonucleotide consisting of from about 12 to about 16 nucleotide bases.

289. The method of claim 271, wherein said probe further includes a label.

290. The method of claim 289, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a nucleotide base sequence region that is unable to stably hybridize to either said analyte or said second nucleic acid under said conditions.

291. The method of claim 290, wherein said label is a chemiluminescent molecule.

292. The method of claim 291, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

293. The method of claim 291, wherein said chemiluminescent molecule is an acridinium ester derivative.

294. The method of claim 289, wherein said label is joined to said probe at a site located within one of said clusters contained in said first nucleotide region of said probe.

295. The method of claim 271, wherein said analyte consists of RNA.

296. The method of claim 295, wherein said RNA is rRNA or tRNA.

297. The method of claim 295, wherein said sample further contains DNA.

298. The method of claim 271, wherein said analyte consists of DNA.

299. The method of claim either 271 or 289, wherein at least one of said analyte, said probe and said second nucleic acid is directly or indirectly immobilized by a solid support.

300. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said probe with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions; and

iii) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said third nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe and said third and fourth nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to either said second nucleotide region of said third nucleic acid or said fourth nucleic acid under said conditions,

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said probe under said conditions,

wherein said fourth nucleic acid is unable to stably hybridize to said first nucleotide region of said third nucleic acid under said conditions, and

wherein said first nucleotide region of said third nucleic acid is unable to stably hybridize to said fourth nucleic acid under said conditions;

b) subjecting the components of step a) to selective hybridization conditions; and

c) detecting said probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

301. The method of claim 300, wherein said probe further includes a label.

302. The method of claim 301, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

303. The method of either claim 300 or 301, wherein said fourth nucleic acid is immobilized by a solid support.

304. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said analyte with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions; and

iii) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said third nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to either said second nucleotide region of said third nucleic acid or said fourth nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte and said third and fourth nucleic acids under said conditions,

and

wherein said first nucleotide region of said third nucleic acid is unable to stably hybridize to said fourth nucleic acid under said conditions;

b) subjecting the components of step a) to selective hybridization conditions; and

c) detecting said probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

305. The method of claim 304, wherein said probe further includes a label.

306. The method of claim 305, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

307. The method of either claim 304 or 305, wherein said fourth nucleic acid is immobilized by a solid support.

308. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said analyte, which comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said analyte with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions;

iii) said probe with said third nucleic acid, wherein said third nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions; and

iv) said third nucleic acid with a fourth nucleic acid, wherein said fourth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a third nucleotide base sequence region of said third nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe, said second and third nucleotide regions of said third nucleic acid, and said fourth nucleic acid under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte, said first and third nucleotide regions of said third nucleic acid, and said fourth nucleic acid under said conditions, and

wherein said first and second nucleotide regions of said third nucleic acid do not stably hybridize to said fourth nucleic acid under said conditions;

b) subjecting the components of step a) to selective hybridization conditions; and

c) detecting said probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

309. The method of claim 308, wherein said probe further includes a label.

310. The method of claim 309, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

311. The method of either claim 308 or 309, wherein said fourth nucleic acid is immobilized by a solid support.

312. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said sample, which comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said probe with a first coupling nucleic acid comprising a third nucleic acid, wherein said first coupling nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions;

iii) a second coupling nucleic acid comprising a fourth nucleic acid with a fifth nucleic acid, wherein said fifth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said second coupling nucleic acid under selective hybridization conditions; and, alternatively,

(a) said first coupling nucleic acid with said second coupling nucleic acid, wherein said second coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said first coupling nucleic acid under selective hybridization conditions; or

(b) one or more optional coupling nucleic acids, other than said first and second coupling nucleic acids, wherein each of said optional coupling nucleic acids is able to stably hybridize to at least two other coupling nucleic acids under selective hybridization conditions, wherein at least one of said other coupling nucleic acids may be at least one of said first and second coupling nucleic acids, and wherein each of said other coupling nucleic acids is directly or indirectly joined to said probe and said fifth nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe, said first and second coupling nucleic acids, said fifth nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said fifth nucleic acid is unable to stably hybridize to any of said first coupling nucleic acid, said second nucleotide region of said second coupling nucleic acid, and any of said optional coupling nucleic acids under said conditions

wherein said first coupling nucleic acid is unable to stably hybridize to said first nucleotide region of said second coupling nucleic acid under said conditions, and

wherein said second coupling nucleic acid is unable to stably hybridize to said first nucleotide region of said first coupling nucleic acid under said conditions;

b) subjecting the components of step a) to selective hybridization conditions; and

c) detecting said probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

313. The method of claim 312, wherein said probe includes a label.

314. The method of claim 313, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

315. The method of either claim 312 or 313, wherein said fifth nucleic acid is immobilized by a solid support.

316. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said sample, which

comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said analyte with a first coupling nucleic acid comprising a third nucleic acid, wherein said first coupling nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions;

iii) a second coupling nucleic acid comprising a fourth nucleic acid with a fifth nucleic acid, wherein said fifth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said second coupling nucleic acid under selective hybridization conditions; and, alternatively,

(a) said first coupling nucleic acid with said second coupling nucleic acid, wherein said second coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said first coupling nucleic acid under selective hybridization conditions; or

(b) one or more optional coupling nucleic acids, other than said first and second coupling nucleic acids, wherein each of said optional coupling nucleic acids is able to stably hybridize to at least two other coupling nucleic acids under selective hybridization conditions, wherein at least one of said other coupling nucleic acids may be at least one of said first and second coupling nucleic acids, and wherein each of said other coupling nucleic acids is directly or indirectly joined to said probe and said fifth nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said first coupling nucleic acid, said second coupling nucleic acid, said

fifth nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte, said first and second coupling nucleic acids, said fifth nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said fifth nucleic acid is unable to stably hybridize to any of said first coupling nucleic acid, said second nucleotide region of said second coupling nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said first coupling nucleic acid is unable to stably hybridize to said first nucleotide region of said second coupling nucleic acid under said conditions, and

wherein said second coupling nucleic acid is unable to stably hybridize to said first nucleotide region of said first coupling nucleic acid under said conditions;

b) subjecting the components of step a) to selective hybridization conditions; and

c) detecting said probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

317. The method of claim 316, wherein said probe further includes a label.

318. The method of claim 317, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

319. The method of either claim 316 or 317, wherein said fifth nucleic acid is immobilized by a solid support.

320. A method for detecting the presence or amount of an analyte comprising a first nucleic acid in a sample suspected of containing said sample, which comprises the steps of:

a) contacting the following components:

i) said sample with a probe comprising a second nucleic acid, wherein said probe contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said analyte under selective hybridization conditions;

ii) said probe with a first coupling nucleic acid comprising a third nucleic acid, wherein said first coupling nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said probe under selective hybridization conditions;

iii) said analyte with said first coupling nucleic acid, wherein said first coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under selective hybridization conditions;

iv) a second coupling nucleic acid comprising a fourth nucleic acid with a fifth nucleic acid, wherein said fifth nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said second coupling nucleic acid under selective hybridization conditions; and, alternatively,

(a) said first coupling nucleic acid with said second coupling nucleic, wherein said second coupling nucleic acid contains a second nucleotide base sequence region able to stably hybridize to a third nucleotide base sequence region of said first coupling nucleic acid under selective hybridization conditions; or

(b) one or more optional coupling nucleic acids, other than said first and second coupling nucleic acids, wherein each of said optional coupling nucleic acids is able to stably hybridize to at least two other coupling nucleic acids under selective hybridization conditions, wherein at least one of said other coupling nucleic acids may be at least one of said first and second coupling nucleic acids, and wherein each of said other coupling nucleic acids is directly or indirectly joined to said analyte, said probe and said fifth nucleic acid under selective hybridization conditions,

wherein said analyte is unable to stably hybridize to any of said second nucleotide region of said probe, said first and third nucleotide regions of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said probe is unable to stably hybridize to any of said second nucleotide region of said analyte, said second and third nucleotide regions of said first coupling nucleic acid, said second coupling nucleic acid, said fifth nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said fifth nucleic acid is unable to stably hybridize to any of said first coupling nucleic acid, said second nucleotide region of said second coupling nucleic acid, and any of said optional coupling nucleic acids under said conditions,

wherein said first coupling nucleic acid is unable to stably hybridize to said second nucleotide region of said second coupling nucleic acid, and

wherein said second coupling nucleic acid is unable to stably hybridize to either said first or second nucleotide region of said first coupling nucleic acid;

b) subjecting the components of step a) to selective hybridization conditions; and

c) detecting said probe hybridized with said analyte as an indication of the presence or amount of said analyte in said sample.

321. The method of claim 320, wherein said probe further includes a label.

322. The method of claim 321, wherein said label is joined to said probe at a site located within said first nucleotide region of said probe.

323. The method of either claim 320 or 321, wherein said fifth nucleic acid is immobilized by a solid support.

324. A method of amplifying a target comprising a first nucleic acid, which comprises the steps of:

a) contacting a sample suspected of containing said target with a second nucleic acid, wherein said second nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a first nucleotide base sequence region of said target under amplification conditions, and wherein said first nucleotide region of said second nucleic acid includes one or more modified nucleotides;

b) subjecting the components of step a) to said amplification conditions, so that

i) the hybridization binding affinity between said target and said second nucleic acid is greater than the hybridization binding affinity between said target and an unmodified form of said second nucleic acid, and

ii) the hybridization rate between said target and said second nucleic acid is greater than the hybridization rate between said target and an unmodified form of said second nucleic acid; and

c) incubating the components of step a) under said amplification conditions, such that said target is amplified.

325. The method of claim 324, wherein said first nucleotide region of said second nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

326. The method of claim 324, wherein said first nucleotide region of said second nucleic acid includes one or more clusters of at least about 6 modified nucleotides.

327. The method of claim 324, wherein said first nucleotide region of said second nucleic acid includes one or more clusters of at least about 8 modified nucleotides.

328. The method of claim 324, wherein substantially all of the nucleotides

contained in said first nucleotide region of said second nucleic acid are modified.

329. The method of claim 325, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

330. The method of claim 325, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

331. The method of claim 325, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

332. The method of claim 325, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

333. The method of claim 325, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

334. The method of claim 333, wherein said propyne substitution is to a cytidine analog.

335. The method of claim 333, wherein said propyne substitution is to a thymidine analog.

336. The method of claim 325, wherein each said modified nucleotide of one or more of said clusters of said first nucleotide region of said second nucleic acid contains the same modification.

337. The method of claim 336, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

338. The method of claim 324, wherein said second nucleic acid includes one or more conjugate molecules.

339. The method of claim 325, wherein said second nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to said second nucleic acid at a site located within one or more of said clusters contained in said first nucleotide region of said second nucleic acid.

340. The method of claim 325, wherein said contacting step further includes contacting said second nucleic acid with nucleotide triphosphates and at least one nucleic acid polymerase.

341. The method of claim 340, wherein said second nucleic acid is capable of having nucleotide bases added to its 3' terminus by at least one of said polymerases.

342. The method of claim 325 or 341, wherein said contacting step further includes contacting said target with a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said target under selective hybridization conditions,

wherein said second nucleic acid is unable to stably hybridize to either said second nucleotide region of said target or said third nucleic acid under said hybridization conditions, and

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said target under said conditions.

343. The method of claim 342, wherein the formation of a stable hybrid between said third nucleic acid and said target under said conditions reduces or prevents amplification of said target.

344. The method of claim 342, wherein said first and second nucleotide regions of said target constitute substantially the same nucleotide region.

345. The method of claim 342, wherein said first nucleotide region of said third nucleic acid includes one or more modified nucleotides.

346. The method of claim 342, wherein said first nucleotide region of said third nucleic acid includes one or more clusters of at least about 4 modified nucleotides.

347. The method of claim 342, wherein substantially all of the nucleotides contained in said first nucleotide region of said third nucleic acid are modified.

348. The method of claim 347, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

349. The method of claim 347, wherein each said modified nucleotide of one or more of said clusters contains the same modification.

350. The method of claim 349, wherein said modification consists of a 2'-O-methyl substitution to the ribofuranosyl moiety.

351. The method of claim 342, wherein at least one of said second and third nucleic acids includes one or more conjugate molecules.

352. The method of claim 346, wherein at least one of said second and third nucleic acids includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to at least one of said second and third nucleic acids at a site located within one or more of said clusters contained in at least one of said first nucleotide region of said second nucleic acid and said first nucleotide region of said third nucleic acid.

353. The method of claim 342, wherein said second nucleic acid contains a 5' nucleotide base sequence region which is unable to stably hybridize to said target under said conditions.

354. The method of claim 353, wherein any of said target and said second and third nucleic acids is directly or indirectly immobilized by a solid support.

355. A kit comprising a nucleic acid probe for use in detecting the presence or amount of a nucleic acid analyte in a sample suspected of containing said analyte, wherein said probe comprises a first nucleotide base sequence region able to stably hybridize to a first

nucleotide base sequence region of said analyte under selective hybridization conditions, and wherein said first nucleotide region of said probe includes at least about 4 modified nucleotide bases, so that

a) the hybridization binding affinity between said analyte and said probe is greater than the hybridization binding affinity between said analyte and an unmodified form of said probe, under said conditions, and

b) the hybridization rate between said analyte and said probe is greater than the hybridization rate between said analyte and an unmodified form of said probe, under said conditions.

356. The kit of claim 355, wherein said first nucleotide region of said probe includes one or more clusters of at least about 6 modified nucleotides.

357. The kit of claim 355, wherein said first nucleotide region of said probe includes one or more clusters of at least about 8 modified nucleotides.

358. The kit of claim 355, wherein substantially all of the nucleotides contained in said first nucleotide region of said probe are modified.

359. The kit of claim 355, wherein at least one of said modified nucleotide bases contains a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage moiety.

360. The kit of claim 355, wherein at least one of said modified nucleotides

includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage moiety.

361. The kit of claim 355, wherein at least one of said modified nucleotides contains a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

362. The kit of claim 355, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

363. The kit of claim 355, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

364. The kit of claim 363, wherein said propyne substitution is to a cytidine analog.

365. The kit of claim 363, wherein said propyne substitution is to a thymidine analog.

366. The kit of claim 355, wherein said probe includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to said probe at a site located within one or more of said clusters contained in said first nucleotide

region of said probe.

367. The kit of claim 355, wherein said probe consists of from about 10 to about 100 nucleotides.

368. The kit of claim 355, wherein said probe consists of from about 10 to about 16 nucleotides.

369. The kit of claim 355, wherein said probe consists of from about 12 to about 16 nucleotides.

370. The kit of claim 355, wherein said probe further includes a label.

371. The kit of claim 370, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent chemiluminescent molecule,
i) a phosphorescent molecule,
j) an electrochemiluminescent molecule,
k) a chromophore, and
l) a base sequence region that is unable to stably hybridize to said analyte under said conditions.

372. The kit of claim 371, wherein said label is a chemiluminescent molecule.

373. The kit of claim 372, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

374. The kit of claim 372, wherein said label is an acridinium ester derivative.

375. The kit of either claim 355 or 370, further comprising a solid support.

376. The kit of claim 375, wherein said probe is directly or indirectly immobilized by said solid support.

377. The kit of claim 355 or 370, further comprising one or more nucleic acid controls.

378. The kit of claim 355 or 370, further comprising one or more hybridization reagents.

379. A kit comprising a first nucleic acid capable of amplifying an analyte comprising a second nucleic acid in a sample suspected of containing said analyte, wherein said first nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte under amplification conditions, and wherein said first nucleotide region of said first nucleic acid includes at least about 4 modified nucleotides, so that

a) the hybridization binding affinity between said analyte and said first nucleic acid is greater than the hybridization binding affinity between said analyte and an

unmodified form of said first nucleic acid, under said conditions, and

b) the hybridization rate between said analyte and said first nucleic acid is greater than the hybridization rate between said analyte and an unmodified form of said first nucleic acid, under said conditions.

380. The kit of claim 379, wherein said first nucleotide region of said first nucleic acid includes one or more clusters of at least about 6 modified nucleotides.

381. The kit of claim 379, wherein said first nucleotide region of said first nucleic acid includes one or more clusters of at least about 8 modified nucleotides.

382. The kit of claim 379, wherein substantially all of the nucleotides contained in said first nucleotide region of said first nucleic acid are modified.

383. The kit of claim 379, wherein at least one of said modified nucleotide bases contains a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage moiety.

384. The kit of claim 379, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage moiety.

385. The kit of claim 379, wherein at least one of said modified nucleotides contains a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

386. The kit of claim 379, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

387. The kit of claim 379, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

388. The kit of claim 387, wherein said propyne substitution is to a cytidine analog.

389. The kit of claim 387, wherein said propyne substitution is to a thymidine analog.

390. The kit of claim 379, wherein said first nucleic acid includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to said first nucleic acid at a site located within one or more of said clusters contained in said first nucleotide region of said first nucleic acid.

391. The kit of claim 379, further comprising a solid support.

392. The kit of claim 391, wherein said first nucleic acid is directly or

indirectly immobilized by said solid support.

393. The kit of claim 392, further comprising nucleotide triphosphates and at least one nucleic acid polymerase.

394. The kit of claim 393, wherein said first nucleic acid is capable of having nucleotide bases added to its 3' terminus by at least one of said nucleic acid polymerases.

395. The kit of claim 379, further comprising one or more amplification reagents.

396. The kit of claim 379, further comprising a third nucleic acid, wherein said third nucleic acid contains a first nucleotide base sequence region able to stably hybridize to a second nucleotide base sequence region of said analyte, such that said analyte is able to stably hybridize to said third nucleic acid under selective hybridization conditions,

wherein said first oligonucleotide is unable to stably hybridize to either said second nucleotide region of said analyte or said third nucleic acid under said hybridization conditions, and

wherein said third nucleic acid is unable to stably hybridize to said first nucleotide region of said analyte under said conditions.

397. The kit of claim 396, wherein the formation of a stable hybrid between said third nucleic acid and said analyte under said conditions reduces or prevents amplification of said analyte.

398. The kit of claim 396, wherein said first and second nucleotide regions of said analyte constitute substantially the same nucleotide region.

399. The kit of claim 396, further comprising one or more hybridization reagents.

400. A nucleic acid probe comprising a nucleotide base sequence region containing one or more clusters of at least about 4 modified nucleotides, wherein said probe includes at least one label joined to said probe at a site located within one of said clusters contained in said nucleotide region.

401. The probe of claim 400, wherein said nucleotide region of said probe includes one or more clusters of at least about 6 modified nucleotides.

402. The probe of claim 400, wherein said nucleotide region of said probe includes one or more clusters of at least about 8 modified nucleotides.

403. The probe of claim 400, wherein substantially all of the nucleotides contained in said nucleotide region of said probe are modified.

404. The probe of claim 400, wherein at least one of said modified nucleotides includes a modification selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

405. The probe of claim 400, wherein at least one of said modified nucleotides includes two modifications selected from the group consisting of:

a) a modification to the nitrogenous base;

b) a modification to the sugar moiety;

c) a modification to the phosphate moiety;

d) a modification to the internucleoside linkage; and

e) a modification to the internucleotide linkage.

406. The probe of claim 400, wherein at least one of said modified nucleotides includes a 2'-modification to the ribofuranosyl moiety selected from the group consisting of:

a) an alkyl substitution;

b) an alkoxy substitution; and

c) a halide substitution.

407. The probe of claim 400, wherein at least one of said modified nucleotides includes a 2'-O-methyl substitution to the ribofuranosyl moiety.

408. The probe of claim 400, wherein at least one of said modified nucleotides includes a propyne substitution to the nitrogenous base.

409. The probe of claim 408, wherein said propyne substitution is to a cytidine analog.

410. The probe of claim 408, wherein said propyne substitution is to a thymidine analog.

411. The probe of claim 400, wherein each said modified nucleotide of one or more of said clusters contains the same modification.

412. The probe of claim 411, wherein said modification consists of a 2'-O-

methyl substitution to the ribofuranosyl moiety.

413. The probe of claim 400, wherein said probe includes one or more conjugate molecules, and wherein at least one of said conjugate molecules is joined to said probe at a site located within one or more of said clusters contained in said nucleotide region of said probe.

414. The probe of claim 400, wherein said probe is an oligonucleotide consisting of from about 10 to about 100 nucleotide bases.

415. The probe of claim 400, wherein said probe is an oligonucleotide consisting of from about 10 to about 16 nucleotide bases.

416. The probe of claim 400, wherein said probe is an oligonucleotide consisting of from about 12 to about 16 nucleotide bases.

417. The probe of claim 400, wherein said probe further includes a label.

418. The probe of claim 417, wherein said label is selected from the group consisting of:

a) a radioisotope,
b) an enzyme,
c) an enzyme cofactor,
d) an enzyme substrate,
e) a dye,
f) a hapten,
g) a chemiluminescent molecule,
h) a fluorescent molecule,

i) a phosphorescent molecule,

j) an electrochemiluminescent molecule,

k) a chromophore, and

l) a nucleotide base sequence region that is unable to stably hybridize to said analyte under said conditions.

419. The probe of claim 418, wherein said label is a chemiluminescent molecule.

420. The probe of claim 419, wherein light is emitted by said chemiluminescent molecule upon the return to ground state of an electronically excited N-acridone.

421. The probe of claim 419, wherein said chemiluminescent molecule is an acridinium ester derivative.